

20	25	30	
Ala Ala Pro Thr Thr Gly Val Val Pro Ala Ala Ala Asp Glu Val Ser			
35	40	45	
Ala Leu Thr Ala Ala Gln Phe Ala Ala His Ala Gln Met Tyr Gin Thr			
50	55	60	
Val Ser Ala Gln Ala Ala Ile His Glu Met Phe Val Asn Thr Leu			
65	70	75	80
Val Ala Ser Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala Ala			
85	90	95	
Ala Ala Gly			

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDELNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Ser Phe Val Thr Thr Gly Pro Glu Ala Leu Ala Ala Rls Ala Ala			
1	5	10	15
Asn Leu Gln Gly Ile Gly Thr Thr Met Asn Ala Gln Asn Ala Rls Ala			
20	25	30	
Ala Ala Pro Thr Thr Gly Val Val Pro Ala Ala Ala Asp Glu Val Ser			
35	40	45	
Ala Leu Thr Ala Ala Gln Phe Ala Ala His Ala Gln Met Tyr Glu Thr			
50	55	60	
Val Ser Ala Gln Ala Ala Ile His Glu Met Phe Val Asn Thr Leu			
65	70	75	80
Val Ala Ser Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala Ala			
85	90	95	
Ala Ala Gly			

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDELNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Asp Pro His Ala Met Arg Asp Met Ala Gly Arg Phe Glu Val His
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Arg Asp Met Ala Gly Arg Phe Glu Val His Ala Gln Thr Val Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Arg Phe Glu Val His Ala Gln Thr Val Glu Asp Glu Ala Arg Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ala Glu Thr Val Glu Asp Gln Ala Arg Arg Met Thr Ala Ser Ala

3

5

10

15

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Asp	Glu	Ala	Arg	Arg	Met	Trp	Ala	Ser	Ala	Gln	Asn	Ile	Ser	Gly
1					5				10				15	

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met	Trp	Ala	Ser	Ala	Gln	Asn	Ile	Ser	Gly	Ala	Gly	Trp	Ser	Gly
1					5				10				15	

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Gln	Asn	Ile	Ser	Gly	Ala	Gly	Trp	Ser	Gly	Met	Ala	Glu	Ala	Thr
1					5				10				15	

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ala Gly Trp Ser Gly Met Ala Glu Ala Thr Ser Leu Asp Thr Met Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Ala Glu Ala Thr Ser Leu Asp Thr Met Ala Gln Met Asn Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ser Leu Asp Thr Met Ala Gln Met Asn Gln Ala Phe Arg Asn Ile
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Aia	Gln	Met	Asn	Gln	Ala	Phe	Arg	Asn	Ile	Val	Asn	Met	Leu	Ris
1					9				10				15	

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ala	Phe	Arg	Asn	Ile	Val	Asn	Met	Leu	His	Gly	Val	Arg	Asp	Gly
1					5				10				15	

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Val	Asn	Met	Ile	His	Gly	Val	Arg	Asp	Gly	Leu	Val	Arg	Asp	Ala
1					5				10				15	

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Gly	Val	Arg	Aap	Gly	Leu	Val	Arg	Aap	Ala	Aan	Aan	Tyr	Glu	Gln
1					5					10			15	

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Leu	Val	Arg	Aap	Ala	Aan	Aan	Tyr	Glu	Gln	Gln	Gln	Ala	Ser	
1					5				10			15		

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Aan	Aan	Tyr	Glu	Gln	Gln	Gln	Gln	Ala	Ser	Gln	Gln	Ile	Leu	Ser	Ser
1					5					10			15		

(2) INFORMATION FOR SEQ ID NO:50:

- (ii) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Asp Ala His Gly Ala Met Ile Arg Ala Gln Ala Ala Ser Leu Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Ile Arg Ala Gln Ala Ala Ser Leu Gln Ala Glu Ala Glu Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:

- (D) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:
- | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Glu | His | Gln | Ala | Ile | Val | Arg | Asp | Val | Leu | Ala | Ala | Gly | Asp |
| 1 | | | | 5 | | | | | 10 | | | | 15 | |
- (2) INFORMATION FOR SEQ ID NO:57:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:
- | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Val | Arg | Asp | Val | Leu | Ala | Ala | Gly | Asp | Rhe | Trp | Gly | Gly | Ala |
| 1 | | | | 5 | | | | | 10 | | | | 15 | |
- (2) INFORMATION FOR SEQ ID NO:58:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:
- | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ala | Ala | Gly | Asp | Phe | Trp | Gly | Gly | Ala | Gly | Ser | Val | Ala | Cys | Gly |
| 1 | | | | 5 | | | | | 10 | | | | 15 | | |
- (2) INFORMATION FOR SEQ ID NO:59:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:
- Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu Phe Ile Thr
1 5 10 15
- (2) INFORMATION FOR SEQ ID NO:60:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:
- Gly Ser Val Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn
1 5 10 15
- (2) INFORMATION FOR SEQ ID NO:61:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:
- Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu
1 5 10 15
Gin Ala
- (2) INFORMATION FOR SEQ ID NO:62:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (iii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:
- Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala Asn Ala His Gly Gln
1 5 10 15
- (2) INFORMATION FOR SEQ ID NO:63:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (iii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:
- Ile Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala
1 5 10 15
- (2) INFORMATION FOR SEQ ID NO:64:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (iii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:
- Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Lys Val Gin Ala Ala Gly Asn Asn Met Ala Gin Thr Asp Ser Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Gly Asn Asn Met Ala Gin Thr Asp Ser Ala Val Gly Ser Ser Thr Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Asp Ala His Gly Ala Met Ile Arg Ala Leu Ala Gly Leu Leu Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Amp Ala His Gly Ala Met Ile Arg Ala Gln Ala Gly Leu Ileu Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Ile Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Gln Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Ile Arg Ala Gln Ala Gly Leu Leu Glu Ala Glu His Gln Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile Ser Asp Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile Arg Asp Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Ala Glu His Gln Ala Ile Ile Ser Asp Val Leu Thr Ala Ser Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ala Glu His Gln Ala Ile Ile Arg Asp Val Leu Thr Ala Ser Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Ile Ile Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala
1 5 10 15

(3) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ile Ile Arg Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Leu	Thr	Ala	Ser	Asp	Phe	Trp	Gly	Gly	Lys	Gly	Ser	Ala	Ala	Cys	Gln
1					5				10					15	

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: peptide

(vii) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Phe	Trp	Gly	Gly	Ala	Gly	Ser	Ala	Ala	Cys	Gln	Gly	Phe	Ile	Thr
1						5			10				15	

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: peptide

(vii) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Gly	Ser	Ala	Ala	Cys	Gln	Gly	Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn
1						5			10				15	

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Gln	Gly	Phe	Ile	Thr	Ser	Leu	Gly	Arg	Asn	Phe	Gln	Val	Ile	Tyr
3				5					10				15	

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Val	Thr	Thr	Asn	Phe	Phe	Gly	Val	Asn	Thr	Ile	Pro	Ile	Ile	Asn
1				5					10				15	
Glu	Ala	Asp	Tyr	Leu	Arg	Met	Trp	Ile						
20								25						

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Asn	Glu	Ala	Asp	Tyr	Leu	Arg	Met	Trp	Ile	Gln	Ala	Ala	Thr	Val	Met
1				5					10				15		
Ser	Bis	Tyr	Gln	Ala	Val	Ala	Mis	Glu							
20								25							

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ANALYSIS OF POLYNUCLEOTIC EXONS: SENS

(xi) SOURCE: DESCRIPTION: SWO ID NO: 83:

TGAGCGCTAA	CCTTACGGTC	GTTTCTGTAC	ACCGAACGCC	TGGCTCTTC	CCGGGACTGC	65
CGCTAGGTC	GGGGGATCACT	CGGGCTTCCC	GGGGCTTCCC	CGGGGGATCA	GGGGGGCTTC	120
ACAGTGTGTC	TGCGGCCCGG	CGATCGGGCG	GATAACGGCC	TGACCTCTAGC	TGCGGCCGAAA	180
TGACAATGCT	CGCTTAAAGCC	TGAGGACTTC	AAGACGACTA	AACGAGGAAT	CGCTTAAAGCC	240
TTTGAGTACATC	CGAACATGAA	GGCTCTTCCC	CGGGGGCGCA	CGGGGGCGCA	CGGGGGCGCA	300
CGCGATGAA	CGCCCGAATG	GGGGTTGGG	CGACTTCCAC	ACGCGGGGTC	CGGGGGCGCA	360
CGGGATGAA	NTGGGGGGCG	TGAGGCTGGC	TGAGTTGGC	CGAACACGCC	AGATCTTATCA	420
GGCGCTGAGC	GGCCCGGGCG	GGGGGATTCG	CGGGGGATTC	TGACACGCC	AGATCTTATCA	480
CTTCAGGCTCG	TTAGCTCTCA	GGGGGGCGCC	CGACGGGGCG	TGCAACACTC	TGCGATGAG	540
CTGGCGATGGA	TTTTGGGGGG	TGCGGCCGCG	AGGGTCTTTC	GGTGGGGGAT	AGGGGGGGTC	600
CTGCATGAGC	ACCAATGGTC	GGTCGGCGGT	GGGGCTGGAA	GGGGTTGGCT	GGGGGGGGCA	660
GTTCGGGGCG	CTGGGGGGTC	GGGGGGCGGT	TGACGGGGAA	TGACGGGGTC	GGGGGGGGCA	720
GTCCGGGGCGTC	ACGGGGGGAT	GGGGGGCGGT	TGCGGGGGTA	TGTTGGGGTG	AGGGGGGGCA	780
CTGGGGGGCA	AGGGGGGGCA	GGGGGGGGCA	AGGGGGGGCA	GGGGGGGGCA	GGGGGGGGCA	840
GGGGGGGGTC	CGGGGGGGTC	GGGGGGGGTC	GGGGGGGGTC	GGGGGGGGCA	GGGGGGGGCA	900
AGCTGATTC	GAAGGAGATTC	TTGGGGTCAA	ACACCTGGGG	GGGGGGGGCA	GGGGGGGGCA	960

22 INFORMATION FOR SDO ID NO. 84:

IV.2. SENSENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

iii) MUSCULAR TYPE: peptides

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Ser Phe Val Thr Thr Gln Pro Glu Ala Leu Ala Ala Ala Ala

122 INFORMATION FOR SDO IN NO. 95:

(ii) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

MOLECULE TYPE: *trans*-*cis*

(ext) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Thr Glu Pro Glu Ala Leu Ala Ala Ala Asn Leu Glu Gly
1 2 3 4 5 6 7 8 9 10 11 12

(2) INFORMATION FOR SGD ID 80146.

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Leu	Ala	Ala	Ala	Ala	Asn	Leu	Gln	Gly	Ile	Gly	Thr	Thr	Met
1						5			10				15

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Ala	Asn	Leu	Gln	Gly	Ile	Gly	Thr	Thr	Met	Asn	Ala	Gln	Asn	Ala
1					5			10				15		

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Ile	Gly	Thr	Thr	Met	Asn	Ala	Gln	Asn	Ala	Ile	Ala	Ala	Ala	Pro
1						5			10				15	

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Asn Ala Glu Asn Ala Ala Ala Ala Pro Thr Thr Gly Val Val

(2) INFORMATION FOR SEC ID NO: 90

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRAND BONDS: single
(D) TOPOLOGY: linear

MOLECULE TYPE: point

(84) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Ala Ala Ala Ala Pro Thr Thr Gly Val Val Val Pro Ala Ala Ala Asp
3 6 10 13

202 INFORMATION BOX SWO ID NO: 63

- (3) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 15 amino acids
 (B) TYPR: amino acid
 (C) STRANGENESS: single
 (D) TOPOLOGY: +ionic

(14) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Thr Thr Gly Val Val Pro Ala Ala Ala Asp Glu Val Ser Ala Leu
 4 5 10 15

(2) INFORMATION FOR FSGO ID NO: 921:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Pro Ala Ala Ala Asp Glu Val Ser Ala Leu Thr Ala Ala Gln Phe

(2) INFORMATION FOR SRO ID NO:23:

- (1) SEQUENCE CHARACTERISTICS:

 - LENGTH: 45 amino acids
 - TYPE: amino acid
 - STRANDEDNESS: single
 - TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Glu Val Ser Ala Leu Thr Ala Ala Gln Phe Ala Ala His Ala Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Thr Ala Ala Gln Phe Ala Ala His Ala Gln Met Tyr Gln Thr Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Ala Ala His Ala Gln Met Tyr Gln Thr Val Ser Ala Gln Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Met Tyr Gln Thr Val Ser Ala Gln Ala Ala Ile His Glu Met Phe
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Ser Ala Gln Ala Ala Ala Ile His Glu Met Phe Val Asn Thr Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ala Ile His Glu Met Phe Val Asn Thr Leu Val Ala Ser Ser Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Phe Val Asn Thr Leu Val Ala Ser Ser Gly Ser Tyr Ala Ala Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Val Ala Ser Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Asn Alan

(3) INFORMATION FOR SEQ ID NO:101.

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

1111 MOLECULE TYPE: protein

(X4) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala Ala Ala Ala Gly
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15

(2) INFORMATION FOR SEC ID NO. 1021

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1784 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

MOLECULE TYPE: cDNA

(xx) SEQUENCE DESCRIPTION: SEQ ID NO:192:

CACACACGCA	CAGCTGACCA	GCGGGGTGAC	TCTTGTGTCG	GGCGCGTCGA	CGAATGAACT	2560
CACCGAGGAA	CAGATGCGAA	ACGGCTCCCG	CGTTTGCGAA	GGGTTGCGGAA	CGAGGACGCC	1525
ACGGGTCTG	CAGTCGCGG	CGTCGCTGCT	GGGTGGGGCG	CTGAGATGCG	TOAAGGACAC	1680
CCGGCCACCG	ACCRACCAAC	TCCTGGTTGT	CGCGTCGACC	AATGACGCGG	TCGGCTGGG	1745
TGTTTGAAAG	TCTACGCTGC	CGCTCTGGTG	GGTACGGTCG	ATTC		1746

(2) INFORMATION FOR SRO ID NO:102:

(1) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(S-1) MOLECULAR TYPE: cDNA

(8) SEQUENCE DESCRIPTION: SEQ ID NO:103:

AACAAACACT	CCTGGTACCGC	GTTGCGGCC	TGATCCCG	TGATCACCTT	GTGTCGAA	60
TGGCAACAG	GTGCGGCCTP	CCCKAAGT	TCTTCGCC	KTGTCGCG	KAATCTCT	120
ATCTGTTG	GGTGGCGCTC	CCCCAAGACC	SGGAGCTTA	ACGATTTA	ACGCGGAG	180
AAGTTTCTTA	CATYTAUCCN	RISMANCCAA	CGGGGCGC	AAAANATCCG	TCTCYGANTC	240
CGGGCGGTT	CGGTGTTCTC	CCCGACCTGT	GAGCGCCG	GARTATCGC	AGGGCGCTT	300
GGGCAACGCG	TCTTGGTAAAC	TGGTCAAGG	TGCGACG	GGCGCATTA	CGGGCTTGA	360
GTCCGACCA	TGACTTCATA	CTGGCGCCA	CACCAAGCC	CGAGCCWAC	TGTCGTCG	420
CGATTCATG	CGCGCGCGCG	CGGCGCTG	ACGGATTG	CGAARRCAT	CGHAGGGRAT	480
TCTATCAUGA	CGGTCACTGG	AAAGGATCG	CCAAATGG	GGAGAACCCN	AGGGACCCGN	540
ATTACGCTT	AAACAGCTT	GGTAGGTC	TTGATGATC	AKRACCACT	AGGGACCGN	600
CGGGCGAAGT	GTAGACCCAC	ACCAAGTCCC	NCAGGTTG	CGCACTTT	GTGTCGCCC	660
GGGATGATG	TAACCGGCG	TTTCTTCTT	ATCGGAGAT	GGGGTGAC	AGGCGGGTT	720
ACGCTTGAT	CGGGTTCCTC	CACTGGCAAG	TGGGGCGCT	CGGGCT	CGGGCT	780

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1311 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CGGCAAGGAA ATGGTCTGGT TCGCTGTGATA GCGATTTGGC TGTGTCGCGA GTCGACGGGU 66
 TGTCAGGAGG TCGCTCTGTC CAGCCCGATG GGGGGGGGGG GGAAGCGGGAT GTTGCGGCGA 120
 CCTCGGTGTAE GAGAACCGGA CTGAGACAGG AGTTCGGCGGT GAGCGCGCGGT CAGTCGCGG 188
 CAGCGGCGGG GATTCCTGGT GCGCTGAGG CGCGCGCGCG GCGGAACTTCAG GAGATGTTCG 240
 TCAAGACTCT CAUAAUHAGC TGGGGCTGCT ATGGCTCTAG CGGGCGCGCG CGGGCGCGCG 300
 CGGGLGGGCTA GAGGGAGTCAC TGGGATGGAT TTGGGGCGCT TCGCGCGGGG GGTCAATTG 366
 CTGGCGGGAGT ATGGCGGGTTC TCGCTGGCGCA CGGGCGCGCG CTGGCGGGCGT GCGCTGGAGAC 426
 GGCGTGGGCCG CGGGCGCGCG TTGGGGGGGG ACCTGGTTAG AGAGGTGGAT CGCTGGCTTC 480
 ACGAGTGGAU CGTGGCTGAGG TCGGGCGCGT GCGGCGCGATG CGGGCGGGATG TGCGCGCTAT 546
 GTGGCGGGCGA TGTAGCTGGCGC TTGGGGCGCGA CGGGCGCGCG CGGGCGCGAC GCGGCGGGCG 609
 CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGGGCG 660

AACCGGGGTT	CCTTGATGCA	GCTGATTCU	ACGAAUGTGT	TTGGTCTGAGA	CACUUCGGG	720
ATCCGGGCGG	CGGAAGCTCA	CTGACGGGAG	ATGUGGUCCC	AGAUCCUC	GGGGATAT	780
GGUACAGGGG	GGAGGTTGGC	GCGGCGGCG	GGGTGACCG	CGTTTACAGC	GGGGGGCG	840
ATTGCGCAAC	CGAACGCTCA	GGGTACGCCG	GGCGGCGGCG	TGGCCACCGC	CGGGGTTAC	900
GGCGATGCG	GGCTGAGCGA	GATGATTCACG	GGUAGTACCCA	AUGGCGTCA	AAAGGTCGAC	960
TAACGTTCTGT	TACGCTGTTT	TACGGCTGCG	CTCTCTGCG	TTCGGCATG	CTTGGTGGK	1020
ACGGCCCAATT	TUCCCACTT	ATTTTGCGCA	CTCTTGACCG	ACGCGACCG	CTGGGGAGG	1080
TCTTNTTATA	ACACCGAAGG	CGTGCGGTCAC	TGAGGACATG	GUATGGGCAA	CAACTTCAFT	1140
CACTGGGGCA	AGACAGCTGGG	ATTGATCGGC	TAGGGGCKAC	CGGCGTGGGT	CGGGGGTGTG	1200
GGGGATTCGG	CCAAAGGGTT	CCGCGGCG	GG			1260

(2) INFORMATION FOR SEQ ID NO:308:

3.2. SPOROCYTE CHARACTERISTICS:

- (A) LENGTH: 2041 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

CASE REPORTS: TYPICAL AND ATypical

(x12) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GGGCAAGGAC	TGTGCCATT	GACCGCTTGT	AUGRCCTTC	GGGNNYTGUA	60
ATACCCACAA	AAKGKKTAT	CTTCTTTG	TCAGTAAAT	ATTTCDDAAA	120
GGACTGGCAG	CAGCTTTCC	GGGTGATGCG	TGTGTTGGT	CGCGCGGGA	180
GGCAAAACCC	GCACACTAGC	GTATTTCCTC	CGGAGCTGG	CGAGACCTGCA	240
ATGCGCTTGA	TCCACGACCA	GGCCACAGCG	GTCCACAGCA	CTTCGGGGGC	300
GGCGAAGGAA	GTGCGAGTT	CGTGGGAGG	GTGKCTTGGT	ACTCTGCTA	360
GTGGGGCGAC	CGCTTATGGC	CGCTCTTCCAN	GGCCGTTTT	CATGGGGCGTC	420
GTGGGGGGGG	CGCTTGGCTA	CGTGGTGGT	AAACACGTA	TCACGGCGAC	480
AAATTGCTT	CCAATTGGC	GGGTGTTGTC	CGCGCGCCCA	TGCGGAGAT	540
GTGGGGGAGCA	TCATCGAGG	CGTGGGAGGA	GAATGTTGG	AGTCATCAC	600
AAAGGCGCTG	AAGAGCTTTC	GGACAACTG	AUGGGGTTGGG	TAACGGGAT	660
GGGTGCTGAA	ACCTGGAGTC	CTTCTTGGC	GGGTTGGCG	GTTCGACGCT	720
GGCTTCTTCC	AAGTCGAGTC	CGTGGTGGT	GGGCGGGGGT	CGGACACAC	780
GTCACGGGGG	ATAGGCTTCA	GGGTTGACCC	AGCTTGGCGG	CTTGGGGCG	840
GGGTGCGGTT	TTGGGGGCTT	GGCGGAGGTT	CGTCAAGTC	ATGCGCGAC	900
GGGGCTTACGG	CGGAGGCTGA	YGKGGGCGT	GGGCGGGCGT	CGGGCGGCG	960
TCGGAGCTGG	TCTGGCGCA	GGGTTCCTAA	GGTATGGGG	GAACGGTGG	1020
ATGGACCCCT	CTTCGGGGGG	GTGAGAAGG	ACACGGACGA	AGAAATCTTC	1080
GGGGCGGCGA	CTGAGAACG	CGAGGGCGG	CGTAGGGAG	CGTGGGGCGA	1140
AAAGGTTCTGG	TAGGAAACGT	CGTCTAACGG	CGTGGGGAG	ACATCCGTT	1200
GGTACACAC	GCGAACTGT	TAACGGGAGG	GACGAGGCA	ATGAGGGAAA	1260
CGACCGGAG	CGTCTGGT	TCTTGGCGIC	CGGGCATGAC	ATGGACGCT	1320
CTGGGGGGTC	GAAGCTCGG	CGTGGCTGG	CGGGCGGAG	TCAGTCGTC	1380
CTGGCTACAG	TCACAACTCA	CGTGGGATGT	GGGGACAAATG	CGTGGGGCTC	1440
GTCTCTTCTAT	ACGCGGCGT	TCGTTGGT	CGAATGCTT	CGTGGGGCGG	1500
TAGCGGGCGC	GGGAGGCGT	GGCGCGAAAG	TATGGGGGG	GGGGCGGTT	1560
GTGTGGCGCA	GTGCAAGGCC	CGACCTAGG	CGGGCTGT	CGTGGGGATCG	1620
ACGGCGGCG	ACGCGGACCC	GGTGGCGACG	GGGGGGCGAC	CGGGCGGAT	1680
CGGGCGGCG	GGTGGCGACG	CAACGGGG	CGGGGGCGG	GGGGCGGAG	1740
GGAGGCCAAC	GGCGCAACGG	CGGTTAACCA	GGGGGGCGG	GGGGCGGAG	1800
TTGGGGGCTG	CGTGGGGGT	CGGGGGCGT	GGGGGGCGG	GGGGCGGAG	1860
ATGGGGGGCG	GGGGGGCGA	CGGGGGCGA	GGGGGGCGG	GGGGGGCGG	1920

TGCTTGTCGA	TGAGATGACTG	CGAACATGCC	AACGAGCAGG	GCATCCGCC	GGCTTGCGGA	1980
ATTGGTGCAG	CGCGCTTGTTG	GGCGAGCTGTG	CGAGCTYTG	CATUCCATCC	ACCTGGTCC	2040
G						3091

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GAGCTCAAG	CTATCAAACA	ATACTTCTG	CACTCCAAA	TGCGGGACAA	CTGGGGTTTT	46
ACCGAAGCTG	CGGUCCACAC	CGCGCGGGAG	TGTTTCAGC	AAATGGCGCA	CCCGAGGAGA	120
ATCGGCGATC	GCATGATTTG	GTGTTGGTGT	TGGCGGAACT	ACCGGGCAT	CGGGTGTGTT	180
CGTATCGGCC	GAAGCTCTCG	CGAACATTT	GAGGCGGAT	TGGCGATGGA	ATACGACCTG	240
TTGATAGTC	TCAGGCCAGG	AAATGCTCAT	TOCCCGGAGA	AACTGGACAC	CACCAAGCCC	300
GTACTCTCG	AGGAAATGCT	TGCGAGCGAG	GAAGAACACA	TGCTACTTCT	GGAAAGCGAG	360
CTGAGCTTGA	TGGACAACTG	AGGAGGGAG	CTTACTCGG	CGCTGTTGCT	CTCTCGGCCA	420
CCGACCTGAT	GGCCGCTTGA	GGATTTCUGG	ATACCACTCC	GGGGCGCGCT	GACAGACCTG	480
AGACATGACT	CGAACAGGGA	TGGAGGCGG	CGATAGGGG	GGGGCACAGC	ACGGACCACT	540
GGCCCCACCG	CAATCGGAGC	CGGTGGGCC	CGTGTGCGTC	CGTGTGCGAC	CACGTTATT	600
TTAACCGGAC	TTGGTTTGGG	GGTGTGCGTC	GTGCGAACCG	GGCGAACCAT	CTGGTGCGGC	660
GCATTCGCCA	CGATGCGTC	CGAGCTGGC	ACGAGCTTGG	GGCGGTGTC	GGCGGTGACC	720
AGCTATCTCG	TTGGGGGAGAC	ACTSKYKKK	KIGEKGKSKS	KRMRMHECTC	GTGATGTCG	780
TGGCGCGCA	CAGGGTGTCT	CTAGGCTCCG	TGTTGGGTTT	CTGCTGTTGC	TCTGTGCTGT	840
GGGGGTTATC	CGACAGATG	ACCATCTCG	CGATCTCG	CGACATVCA	GGCGTGTGCG	900
CGGGTGTGAT	TTCCGTCGAC	GGCTACCGC	TGCGGGCTGA	GGTGTGCGCA	CTGGGGAGAC	960
GTGGCGCGTA	CGAAGGGGTC	TTATGTTGGG	TGTTGGGTGT	CAACACGTC	ACCGGTCGCC	1020
TGCTGGGGGG	CGATCTCTCA	GTGCGGGTGT	GGCGTTCCGA	CCACCAAGCC	1080	
CATACGGGAC	CGAGGGGGGG	TCTACGGGCG	GAACAGCGGC	CTGGGGGGGT	1140	
TCCTTGGGG	AACGTGTTGTC	CACAGGCCA	GAACGCTGAA	AAATGCGATG	GGCGAGCCAC	1200
AC						1260

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GGCGGGCGCA	GTTCGGCCAGC	AGTINCGCGG	GGGGAGCCGG	TTGCGRNAGCC	AAAGAATCGG	65
CTCTGGCGCA	CAGCGGGGAC	CGCGACCGCT	GTGCGTGGT	GAACGCGGGG	ACCGCGCGCG	120
ACCAAGCGA	TTCGCGGCT	GAGGAGTCG	GAANTGNTGG	CACTGATGAC	GGCGTGTGTC	180
ACCGCTTCCC	GGATTCGCGA	CGCGATCGCC	GGCGAAGCCT	GGTGTGCGAC	ACCGCGCGAC	240
ACCCGTAACG	ACAGGGCGGC	ATAGCTTAAT	GAACGCGGGT	NAACCGCGTC	GGCGCGACCG	300

NGANATCGGC	CUGGAGCCTA	AAGTCCGTC	GGGCTCTCCG	TCTGGCGACU	ACAGCCACGT	360
TCACCCCGGC	TTTACCGGTTG	CCCCGCGATG	CATACTGGC	GGCGTCAGG	TNGGCTTGCG	423
GGTAGTCACG	CACACGCG	GTTGATTTGGT	CTATGCCCTG	GACGGGGGGG	GTGACGCTGG	480
GGCGGATCAG	GTGCGAC					

321 INFORMATION FOR SEQ ID NO:102:

4.2. SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TGGATTCGAA	TAGCGTTTCG	GCCCCCTCGA	CGGGGCGACCA	CCTGGCGCGAG	GCCTCCGAAAC	68
GGGGGGCTGG	GACGCTTGGGA	TTCGGGGGG	CUCCAACCAA	RAAACCGGCG	GTGCGGGCGG	120
TGGGGCTGAC	CGCACTGGTG	CUTGATGAGT	GGGGCAACGGG	CCCCGGGGATG	CGATGATGTC	180
CGGGGGACTCG	GGAGGAGGCG	AGCACCGAGC	CGAGGGCGCC	CGACGGATGCG	GGAGAGGGGG	240
GAGGGCAAGG	CTTACCGCGAC	GACACCGAAGT	ACCGGGATTC	GGAAATCACUT	GGGGCCCTAC	300
GUGGCGAAAG	GAGGATGATG	ATGGCGCTTC	TGAGATCTTC	TATGCCACAGG	TTGGGGGCTT	360
CCCCGGTGGC	GTTCGGCGCC	ANAGGGGUGC	TGATGCGGCG	CACCGATGGT	CGGGGGGAGC	420
AGGGGGGGAT	GTGGCTCTGG	GGCTTTCGAA	AGGGGGGGTC	UCCGGGGGG	TTTCGGGGCG	480
CCCCATGGCCC	GGTTGGGGGG	GGGGCGCGCA	AAGTCACACG	CTTGGCTGGAT	GGTTGGGAGG	540
GGAAATTGGG	TGAGGGGCGC	GGTACCTATA	TGGCGGCGCG	TGGTGGCGGG	GGTTGGACCT	600
ATACCGGGGT	CTGATTCGAC	CTCTGGGGCA	GGAGGGACTT	GGTAGCTCGG	AAACGGTATA	660
CGCACTGGCC	GGCGATTTTG	GGATCTGGCG	GGATGGGGCG	GGATGATGCG	GGATGGGGCG	720
GAGGTTGGT	GGCGGAGATCG	GGTGGGGCGA	GGGGGGGTTG	CGAGGTGCGT	GGCAAGGGCGA	780
TACCGGGGGT	ACGTATCAGG	GTGGGGCGGC	ACAGTTGTTAA	GGAGGGCGG	GAAGGATTTG	840
TGGGGGGCTT						900

(2) INFORMATION FOR RPO ID NO: 102:

(2) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) MOLECULAR TYPES: proteins

(x) : SEQUENCE DESCRIPTION: SEQ ID NO:169:

```

Net Seq Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
   1          5           10          15
Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
   20         25          30
Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
   35         40          45
Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys
   50         55          60
Val Asn Thr Ile Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Xaa
   65         70          75          80

```

Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly
85 90 95
Phe

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Ser Leu Ieu Asp Ala His Ile Pro Gin Leu Val Ala Ser Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Ieu Val Ala Ser Gin Ser Ala Phe Ala Ala Lys Ala Gly Leu Met
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(E) MOLECULE TYPE: peptide

(F) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Arg Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly
1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:114:

(I) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(II) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Gln Gln Ala
1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:115

(1) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(II) MOLECULE TYPE: peptide

Yeast endogenous protease - SEQ ID NO:115

Arg His Thr Ile Gly Gln Ala Glu Gln Ala Asp Met Ser Ala Gln

- (12) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Gln Ala Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly
3 6 10 13

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Ala	Met	Ser	Ala	Gln	Ala	Phe	Nis	Gln	Gly	Glu	Ser	Ser	Ala	Ala
1														15

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Ala	Phe	Nis	Gln	Gly	Glu	Ser	Ser	Ala	Ala	Phe	Gln	Ala	Ala	Nis
1														15

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Gln	Ser	Ser	Ala	Ala	Phe	Gln	Ala	Ala	Sis	Ala	Arg	Phe	Val	Ala
1														15

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Phe Gin Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys Val
 3 5 10 15

(2) INFORMATION FOR SEQ ID NO:121:

Sequence Characteristics:

- (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) MOLECULAR TYPE: peptidom

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ala Arg Phe Val Ala Ala Ala Lys Val Asn Thr Leu Ile Asp
 1 5 10 15

(2) INFORMATION FOR SSO ID NO:122:

(a) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANGENESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala Ala Ala Lys Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn
 1 5 10 15

(2) INFORMATION FOR SRQ ID NO:123:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: peptide

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:123;

Asn Thr Leu Leu Asp Val Ala Glu Ala Asn Leu Gly Glu Ala Ala

(2) INFORMATION FOR SEQ ID NO: 1-28

FIG. 8. SEQUENCE CHARACTERISTICS.

- (A) LENGTH: 18 amino acids
(B) TYPE: amino acid

(C) STRANDNESS: single
 (D) TOPOLOGY: linear

(1.1) MOLECULE TYPE: peptide

(8) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Val Ala Gin Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val Ala Ala
 1 S 10 19
 Arg Ala

(2) INFORMATION FOR SSO ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

MOLECULAR TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CCGCGACGAGA	ATGTCTCCCTT	TGGCTTGATA	GCGACTTCTGC	TGTGTGTCTGC	CTTCCTCCACGG	63
GTCAGCGGAG	TGGCGGCTGG	CAGGCGGGCG	GCGCGCGCGG	GAAGCAGCGAT	TGGCTGCAGA	120
CCCGGCTGAC	GAGAACCGGA	CTTGCAACAG	TGGCTGCAGA	TGGCGGCGGT	CAATTGCGCG	140
CACGCCGCGCA	GATCTTAATCG	GCGCTTCCAG	GCGCGCGCGG	GGCGATTTACG	GAATGTTTCG	140
TGAAACACTCT	TCGAGTNNNAC	TCAGGGTCTG	ATGGCTGCG	GAAGGCGGCC	RAACCGCGCC	150
CGCGGGCTTA	GAGGAGTCAT	TGGCGATGGAT	TGGTGGGGCT	TGGCGGCGCA	GGCTCATTTG	160
GTGCGGATTT	ATTCGCGCTTC	TGGCTTGCGGA	CCAAATGTCG	CTTGCGGCTC	GGCTCGGAA	170
GGGTTGGCGG	CGGGGGCTGG	TGGCGGCGCC	ACGGCTTATG	AAAGGCGAT	CTACAGCTC	180
ACCGCTTGGG	GGTGGTCTGG	TGGCGGCGCC	GGCGATGATG	CCGGCGATGT	TGGCGCGAT	190
GTGCGGCTGGA	TGAGTGGCCG	TGGCGGCGCA	GGCGAACAGG	GGGCGACACA	GGCCAGGGCC	200
GCAGCGGCCG	CTTTGGTAGG	GGGTTTGGCC	GGCGACAGG	CTTGCGGCGT	GGAGGCGGCG	210
ACGGCGGCTT	CGCTTGGATCA	CTTGATGATC	GGGCGATGAT	TTTGCGGCGT	GAATGGGGCG	220
ATACCGGGCG	CGGAAATCTA	CTACCGCGAC	ATGGTGGGCC	AAAGACTCCG	GGCGATGTAT	230
GGCTAAAGCGG	GGAGTGTGGC	GGGGCGCCCT	GGGGCGACCG	GGGTTTACAC	GGCGCGCGAC	240
ATTCGCAACG	GGCGCGCTTC	GGGGTACCGG	GGGGCGCGCC	TGGGCGACCG	GGCGCGTACCC	250
GGCCGAGTCGA	CGCTTGACGG	GGGGTACCGG	GGGGTACCGG	GGGGCGACCG	GGCGCGTACCC	260
TGACCTCTCT	TGGCGATGTC	GGGGTACCGG	GGGGTACCGG	GGGGCGACCG	GGCGCGTACCC	270
ACGGCGCAATT	TGGCCCGCTTC	AACTTGGCGCA	CTTGATGACG	GGGGTACCGG	GGCGCGTACCC	280
TINTTINTATA	ACACCGGAGGG	CCTTGCGCTTG	TTCAGGATCG	GGATGGGCAA	CAACTTCATT	290
CAZTGCGGCA	ACAGGCTGGG	ATGATGGGG	TAGCGGCGNC	GGGGTGGGCG	GGGGGCTCTCT	300
GGGGATGCGG	GGGGATGCGG	GGGGGCTCTT	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	310
GGCGAGTCGG	GGGATGCGGG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	320
CGGGTGGCGG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	330
GGCCGGGAGG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	340
GGCGCGCGGG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	350
GGGGATGAGG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	360
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	370
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	380
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	390
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	400
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	410
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	420
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	430
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	440
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	450
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	460
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	470
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	480
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	490
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	500
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	510
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	520
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	530
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	540
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	550
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	560
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	570
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	580
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	590
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	600
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	610
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	620
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	630
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	640
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	650
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	660
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	670
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	680
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	690
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	700
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	710
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	720
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	730
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	740
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	750
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	760
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	770
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	780
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	790
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	800
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	810
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	820
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	830
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	840
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	850
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	860
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	870
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	880
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	890
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	900
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	910
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	920
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	930
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	940
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	950
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	960
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	970
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	980
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	990
GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTCTG	GGGGGCTGGG	GGGGGCTGGG	1000

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Met Asp Phe Gly Ala Leu Pro Pro Glu Val Asn Ser Val Arg Met Tyr
 1 5 10 15
 Ala Gly Pro Gly Ser Ala Pro Met Val Ala Ala Ala Ser Ala Trp Asn
 20 25 30
 Gly Leu Ala Ala Glu Leu Ser Ser Ala Ala Thr Gly Tyr Glu Thr Val
 35 40 45
 Ile Thr Gin Leu Ser Ser Glu Gly Trp Leu Gly Pro Ala Ser Ala Ala
 50 55 60
 Met Ala Glu Ala Val Ala Pro Tyr Val Ala Trp Met Ser Ala Ala Ala
 65 70 75 80
 Ala Gln Ala Glu Gin Ala Ala Thr Glu Ala Arg Ala Ala Ala Ala
 85 90 95
 Phe Glu Ala Ala Phe Ala Ala Thr Val Pro Pro Pro Leu Ile Ala Ala
 100 105 110
 Asn Arg Ala Ser Leu Met Gin Leu Ile Ser Thr Asn Val Phe Gly Glu
 115 120 125
 Asn Thr Ser Ala Ile Ala Ala Glu Ala Glu Tyr Gly Glu Met Trp
 130 135 140
 Ala Gln Asp Ser Ala Ala Met Tyr Ala Tyr Ala Gly Ser Ser Ala Ser
 145 150 155 160
 Ala Ser Ala Val Thr Pro Phe Ser Thr Pro Pro Gln Ile Ala Asn Pro
 165 170 175
 Thr Ala Gln Gly Thr Glu Ala Ala Val Ala Thr Ala Ala Gly Thr
 180 185 190
 Ala Gln Ser Thr Leu Thr Glu Met Ile Thr Gly Leu Pro Asn Ala Leu
 195 200 205
 Glu Ser Leu Thr Ser Xaa Leu Leu Glu Ser Ser Asn Gly Pro Leu Ser
 210 215 220
 Trp Leu Trp Gln Ile Leu Phe Gly Thr Pro Asn Phe Pro Thr Ser Ile
 225 230 235 240
 Ser Ala Leu Leu Thr Asp Leu Glu Pro Tyr Ala Ser Xaa Xaa Tyr Asn
 245 250 255
 Thr Glu Gly Leu Pro Tyr Phe Ser Ile Gly Met Gly Asn Asn Phe Ile
 260 265 270
 Glu Ser Ala Lys Thr Leu Gly Leu Ile Gly Ser Ala Ala Pro Ala Ala
 275 280 285
 Val Ala Ala Ala Gly Asp Ala Ala Lys Gly Leu Pro Gly Leu Gly Gly
 290 295 300
 Met Leu Gly Gly Pro Val Ala Ala Gly Leu Gly Asn Ala Ala Ser
 305 310 315 320
 Val Gly Lys Leu Ser Val Pro Pro Val Trp Xaa Gly Pro Leu Pro Gly
 325 330 335
 Ser Val Thr Pro Gly Ala Ala Pro Leu Pro Val Ser Thr Val Ser Ala

340	345	350
Ala Pro Glu Ala Ala Pro Gly Ser Leu Leu Gly Gly Leu Pro Leu Xaa		
355	360	365
Gly Ala Gly Gly Ala Gly Ala Gly Pro Arg Tyr Gly Phe Xaa Pro Thr		
370	375	380
Val Met Ala Arg Pro Pro Phe Xaa Gly Ile Val Ala Ala Ala Thr Tyr		
385	390	395
		400

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GGCACAGAGCA CCGATTTGACT CGCGAAGAAC CTGACGCGGC CACCCAGCGC CGCCCGCATC	60
ACCGCGCGCG CGCGCGCGAC CTGGCGACAG CTGTTTGGTA AACGUCCAC AC TGCGGGGAG ATGGGTACCG	120
CCCGACCAT TTGGTGTAG GACCACCTCG CGGAATGATG CCTGGAGGGG TGTCCTCGCG	180
CCACACCTG TTGAGACGTC CGCGACCTCG TCTCTACT CGAAGGCTTC TGCCTGCAAG	240
ACACCGGCC ACATGCGCTG TTGCGGATG AGCGGATGCGC CGCGXGGCCC GGATGAACTCG	300
CGTGGCGCC CGTGGCGCC AGCGGATGCGA GGTTGGGCC AGGTGCGCCA GTTGCCGACCG	360
TCTGTCAGCA GCGGAGACAG CGTGGCGCC CGGGCGCTC TGTGCTTGTGAT GACCTGCGAC	420
GAAGATTTCG GACCGACAT GCGGAGCTCC CGAAAGACAA ACTGAGGTCG CTGC	480

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CTGGCGCGCG GAAAATAA TTACTGGCGA GACCGCGAGA ATGCGATGGG ATATTCGCGT	60
GATAGGGCGC CGAAGGAAAC GACTGTGGC AGGGTAAACA CATCGTTTAT TCGTTGCGGT	120
TTAGGTCTTG GATCTCGCG GAOGCAACG ACGTGGAGG AGCGCTCGAG CGAGCGCTGT	180
TGACAGAGTC CGTTTACCGC GAATCTCGCA CGCGTCAGAT CGGAGGATAA CGCACTCGCG	240
CGACACUCA GAGGGCGTGG AGTGGCGGTG CGTGGGTCAC GACCGCGAGC CGTTGGAGAC	300
TGGCAAGCTC AGCGCGCTTC ACCGGACAGG ACCGAACTGGT CGGGTGTGTC CGCGACTGAG	360
CGTGGCGGGG CGCGGGGGTC ATGGCGCGAT CTGCTCGCGT ATGGCGGAGC CGCGCGAGCA	420
GCTGCTCTCG ACTCAACCAT CGGGGGCGTG CGGGCGCTCT CGCGTCAGCA CGCAACGGG	480
TTGGCGGTG CGCTGTTGGT TGAGTCTTCG GAGGGCGCTCG AGCGCGCGTA CGAGCGCGGC	540
CGTGTGTTTC CGAGCTCGC GAGGGCGACAC TTGAGGAGC ATGCTGGCGA GATGGCTTGT	600
CGCTGGCGC GGTTGCGACG TCATCGCGT GGGATATCGA GTGATGCTATC CGCACGAGAC	660
CGCGCGATCG CGCGCGCGCA CGCGCTACAC CGGGTGTCTC CGCTTGACCG CGCGACGACG	720
TACGTGCGCG CGGGCGATCG CACGATATCG ATCGATGACAA CGCGCGCGTG CGGGGGGTGA	780
CTGCGCGCGA TACCAACCG CGGTGTTGCA CGATGAGTC CGCGCGCGCG CTATCACCGT	840

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CAGGTCGGCA CCTTGCGAGT CTGATGGGT CGCTGCACCC TCTCGGACT CGCTCTGGCG	900
GCTTAAGT GGTAGGTCAG GATUICGTC AGCAGCTTG CGTCAGTCTT GAGTTGATCG	960
ATAATGGCGG CGGGCACTT GTGGAATGCG GGTGTTGTTG GGGUAAAAC GGTGACTCG	1020
CGGGCGTGG GGGTGTGUGAC CAGATTCACK TCGGTTTCA GCTTCGCCGA CASASCGAG	1080
GTCAAGTAC TGAGACATCG GGTGTTGCGA GCGCGCTTG CGACCGGTC TTGGCGCAT	1140
CGGGCCACCG ATCGGGGACCG GGTGGGATTT TCGGCCGCTT ATTTCGCCGA CCACATACCA	1200
ATCGGGTCCG CTGGGGTCTCG CGATTTCGGC CGTGGTACCG GGTGCGCGG GGTGTTGCG	1260
CGGTTTCGGG CTGTTGTTCTT CGCACACGGG TTGTTGCTC GAGAACCCG CTAGACACCG	1320
AATCGCGATG GCTGGAGGGC TCGTGTCTCG CGCGGTTTG GCTGAACTG TGTATCTCG	1380
TTCGATTCCT TTGCTTCTCG GCGGGGTTTG AACCGCCCGCC TCGTGGTGG A	1432

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GGACGAGAGT CUTAATCTTG CAOCCCAGGG CGCTTAGGAAA CGCTGGCGT GGTAACTCTA	60
GATGGGGGG CGCTTGGATT CGAGAGTTGA CGATGGGGCG GGGGAAATG GGTGACCGAC	120
CGAGACTGAT TGGCGGGCGAG CGGGCTTGGG CGTGTAACTG CGGGTGGCG CGTGGCGGA	180
ACGGCTTCAC TUCAGGAACTT TCTGAGTACT ACGGACGGA CTTTAACGCA TTATGCTGA	240
CGATCTTGGC CTCCCAAGACG TCCAGAACTC ACTCGGTC	279

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

ACGCCCACTT CGGGCGCGGA ATCACCGTGG GTAACTGGG ATATCAATT CTTCAGGGAC	60
GCTCTGGCGA ACAGCGAACCC CGAGGGCAACG CGTGTAACTG CTTCCTTCTC GATGTCGCA	120
CCGGCGGGGG CGTGGAAAGA AACGATACGA CGGGCGCTCT CGGGGGTCAA CGATUAAATG	180
TGTGAGGGGG CGAGGACAGG CGAGGCTTCA CGGGGGGGCG CAGATTCGCA	240
CGGACCACTAA TGGCCAGGCG GTTGATTTG CGGGCAACG TGAGGGGGAC ACCCTGAAAC	300
TNTTGATGT GTCTACATTG CGGGCTTAC AGCGGGCA ACTCAACCGC GACGGCAAGCC	360
GTGGGACGGG TGCGGTGACG GGTGTTACTC TGTGATATG AGACCTTGG CGCATCACCG	420
CGAGAAATCA TGTTGCTCTG CGTGGACGG CGGGTGGCG CGATGAGGAG ACCGGCGGGG	480
TATTTCAAGG CGACATGGT GGTGCGCGG CGGGTGGCG CGTGGCGGG TGCGGATGCG	540
CGACCGGGCG TGAGCTTTC CGGGAGAAC TCGGGGGCTT GGCGCGCGA GAGCTCAAGT	600
GAAGAAGAT AGTCTACAG CGGGTGGTTC AGAGAGTGA TTAATGGCA GGCGATGCG	660
CGACCGGGCG GTGTGTCG CGGGTGGCG AGCTGGCGC GGCGAAGTC CGGGGGGTC	720
TCTCTGAGGA CGTGGTGGAT TGGTGGCG AGATGCGC TGGCTGGT GAGCTTTGCG	780
CGAGGCTCTT GGCGCGCGAC GGCTCTTCCG CGGGATGCGT CATAGGGCG CGGGGGACCG	840

CCACGCTTGG TCTGCGCTTC CUCCATCAGG GGCCTCTGGT TCTCTATGGC CTTCCTTAAGAAG 903
 GCGCGGGTG CGCGGTACAC AGCCGCTTC TTTCCTGACG CTAGGGGCTCA ACACCAACGCT 960
 TTCCCGCTCT AACUAGGCTT AGGGAGGCTC AGGGGTGAGT TGCTCTACCA GCTCCACGGC 1020
 ACTCTCCAC GANTCCAGCA ADRACACRAC ATGGGGCTTA CTACCCCGCA AGCGCTCAG 1080
 CGCGGAGTT CGAACCTGGC ATTCGGCTTC AGGTGGAAGA TCACCGAGTC CGAGCTTGGC 1140
 GCGGGGATAT CAGCGCGGAA CGCGGAGG CATTGGGGG UGGAATATTC CGCGGGTTC 1200
 GTGCGGGGT TCTCCACGCC ACTCAGCACT TGTTGTTTG GGGACTAAAC GCTTTATCGA 1260
 GCGCGGGCG ACCAGGGCTT TTACAGGGC CTYTCCTGGC CGGACATCGG AGTACTGCG 1320
 GTTGACCGAG TCGAGGGGGG GCGCGGACCA GCTTAAGGGT TCCCGCTCC CGAAACCTTC 1380
 GAGCAGGGC AGTTTGGGCG GCGAGCTGAG CGCTCGGGG CAATCCATCG GGTCACGCTC 1440
 GAGCTGATCC AGCAGCTGTG CCCAGGTTTC 1470

(i) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1059 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

ATTGCGATCG CTGGGGGACG TATCACCAGG TACTCGGTTT CTATGGTTT CGCGCGGGCTT 60
 TCGTTTGGCC TGGGGCCACGG GTCTTCTAGG GGGCGCTTCG TGCGGATGG AATTTTTGAC 120
 AACGAAATCG CGCGATGGGT GAGCATCATCT CGCGATGCGA AGACACGGTT TCGCTQCGC 180
 GGGTCAAGT GGAGGTTTAAAG CGAGGGTACAC AGCTTGACG GGGACACTGG CARACCCCAA 240
 ACCCACACAC CCTGGGACGCR TCGGGCTTCG GGGCGTCAA TTCGGGGTAG ATATGCTATA 300
 CGCGATGGGG ATTCGGTACG CTTATCGAGC CGAGGAGGCGC GCGCTAGACG CGCGGGAT 360
 TCGAGATGG CTGGCGGGACG GGGTGGGGGT CTGGGGGTT CGGGTGTAGG GGTTCGGTC 420
 CATGGATGGT CGGGGAATCT TTGCTCTGGT CGATTCGGT AGGGCTGCTG CGCGGAATGG 480
 GCACGAGATG CGATCCCCA GAAGGCTCA CGGGCTCA ATGGGACATG ATGGTGGAT 540
 CGATGATGAA CGCTCTGCTC AIGCTCTGG CCTATCTCAA CGGTGTTGAA TTCCATGCT 600
 TAGCTTGTG TCTGCTTCTC AGCGTGGGG CCTACAGCTG CGCTCTCTCG CTGGGGCGAT 660
 GTCAAGGGTT TTTCCTATC TAAGGGAGTC CTGAGGTGG AGTGGTCTTA GACGCGAT 720
 TCACCTGGTGG TGCGGATACAT CGTCCTGGCA CATTGGCGCT CCTGGCAACTS CGCTGGGACA 780
 ATGGGGCRAAC CGCGCTGTAG CTGGGGCGA ATTGGGGACG AGGATCCRCG GGAGATGGCC 840
 GACGACTTCG AGGAGGCTCG GATGCTCAAC ACCGTTGGT CCTATCACAA CGAGBAGGCA 900
 AAAGAGAGGCG TCATGCTATCT CGTGGCGGACG GGGACACAGG AGAGGGGGCC CATGGAACTC 960
 GTAAACGAGG TAGACAAAGA GGGACATGAG AGCTGGTCTAC GATGGGGGGC GACGTTTCA 1020
 TACAAGGAGC ATCTTAAGTT TTGATTCGGG AACATCTCA 1080

(i) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GCACAGAGCA TTGGCGGCGA TGTGATAAA CGGTGACGTA TGTGGCACAAA ACAGCCGAGA
GAACTACATG CAGATGAGAAC GTCCTCGGTTG GCTGGTGAAGCC GCAGAAAGTC CGTTCGCCCTC
GGTGTATTTG GACGACTTGC AGGACTCTTG CCG 60
120
153

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:133:

CCGGCGGTC GATCAGCGAG CCAGCGAAA ACTCTGTCGA CGCGAGATCG ATATATTCGCA
CCCGCGGAG CATUTGGCGA AGCATTCACCT CGATGTTCTT GTGUTGATTC GACACAGCTT
GGGCGCGGTA GACTCTCTGG ACCTCGCGAA CCGGGTGTAT CTGCACTCG CGGCGCGGCT
GCACCGCGGCA CACCTCATGC CGGTGGCGCG ACCCTCCATG CCGCTCTCG CGCCCTCGA
GGTGGTGGCC ATGGAGAGAGC ACCCTCGG AACCGCTTC GIGUTGAAAC ACCCGAGCG
GCTCGCGTC GGAGAGCTTG TCGTAGAGCA CTTCCTCAAC GCGCTCGCA GAAACUATGG
TGATCTTGTG GACCGCGCTG CGCTCT 360
387

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GTTCAAGCAAG GCTATCGGAT TGTGGCGTTC GCTTCGCTGG STGCTGAACA CGACGATCGAC
ATCGTGCTCG ACGACGAATC CGCACTCTCG CGACCGCTCC AGTTCCTCGC CGAGAGAGCTG
CTGGCGACCA AAAGACGGTCG UGGCGCTGTC CGTGGGTTGCG GACTGACACC GGTACGCGCC
CCCGACACGC AGTAACTACTG GTTGGCGGAG CGAACGACAA CGACGAGTT TATGGGGCG
CGACCGCGAC ATAACGCGCC AGCGAGGGTG CGCGACGCTG CGCGCGCGCG TATGAGACAC
GGCTATCGAC TGATCTGTC CGACCGCGCA CGCGATCGCA ATTGATGTTG GGTGGGACCG
CGTTCGCGCTG CGACGACCTA AGGGCGCCCC 360
389

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:135:

CCCGCGGTG GATGATGCC COTCTCTTG CGCCGCCATT TATGCTTGT GATGACGTG	60
TGGAGAAC CGGGTTCGC TACCGTGAG CGGAATATC TTGGAGGAG GTCACCGAT	120
GTCACATTA ATTCCTTCC CGCGTGGCG CTTTGCTTG CGGAAACAC GGTGTTGTTA	180
AGCTTGTGCT GTCGCGAAAG AGCTTGGCG CGCTTGCTTG CGAAGATAA TGAGCACCTG	240
ACGTTGGCG CGATGCCCGT TATCCCAAGG ATTTCGGAGG TGCTTCCCG AGATGCCGAA	300
GGGTTCCAGG GTCTGTGTTG CGCTGTGUGG TCGCGTCAAC CACTCGGCCG GGATATGCG	360
AGCCCCCGCG AGCGTGCAC CAGGATCGG CGCCCGCGC GGAGCAGCGT CGQNGCTGN	420
NCCTTCTTC TTNNNGCGAA TTNNNACTCG CGACACANCT TTNNNCCGAC TTNNAUCCUN	480

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GCACGAGCT ACCGGCGGT CGCCGCCAT GCCTCGATG CACCGCTAGC CACGGTINCA	60
TNCAGCGGT CGCGGCCCGC GTCGGGCTT AACGCTATG CAGUTCTAA CAACCTACCG	120
CGCGCAATTA CTTGTGATGT GAACCGATGA CCATTCGCTT CGATGTCAT CGTGTGTTT	180
GGCGCGCGG TATTTGCGCC ATATATTGCTT TTNNNACCG AGCTTAGAC GSTATCGATT	240
CCTTGGCGAC CGACCGCTCA ATTTCAGCA CCTTGGGGG AACATGAGC CGCCCGCGCC	300
GGGGCGTTTG CGAATGTTG CTCAGACG GTGTCGAGG CGACCGCAT GTCGCGGTA	360
GGGACGCGGC GGCTGGGATC GTGCGGGTGA CGCGCGCGT TCTGAALACG AGGGAGGCC	420
CGGGACTCTT AGCGGCGGA CGCGCGCGT GTCAGTCAC TAGGCTACG CGCAGGGGTT	480
GTNTAGCAA CGAGGATGAC KKAATAAAN CGAGGAGAG ACAGNGACG CINCUGANANG	540
CTXANCGCGG TTGCGNCGAA MMHACWCAAC TTNTACCGGG CTTATGNN	587

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

CAGGCATGAG CGACGGCGTC ATCATGATC CAGGATGAG TGCCATTGAC GGCTGTGAC	60
ACCTTCTGG GTTGGAAATC CGCAACCGAG GGCGTATCCT TTACTCTCA CTGACTACT	120
TGCGAAAGC CCTGGAGGAG CTGCGACAG CGTTTGGCGG TGATGGCGG TTAGGTTGG	180
CGCGCGACAA ATACGCGGCG BAAAACCGCA ACCACCGAA TTITTTCCAG QAACTGGCG	240
ACCTGATG TCACTTCATC AGCGTCTGCTT ACAGACCGAC CAAGCGCGTC CAGCGCGCT	300
CGCGACATCTT GGAGGGCGCC LAGAAAGTC TCACTTCATC CGCGCGCGTC CGCTGTGAGCC	360
TGACCTCTAT CGCGCGCGTC CGGCGACCGCC TATCGCGCGC CTTCGCGCGC CGCTTGTGCG	420
CGCGCGCGCG CGCGCGTGTG CGGCGCGCGC TTGGCTACTT GTGCGTGAAG AGCGTCTG	480
ACAGCGCTCA ACTCGCTCAA TTGCTGCGA AATTGGCGGA GTTGGTCCCG CGCGCGATTC	540
CGCGACATCTT TTGCGATGTC CGGCGACATCA TCAAGGAGCG CCTTGGAGAA GTGCGGGAGT	600

TCTATCACAA	CCTGCTCAAC	GCGCTGAAG	AGCTTTGGAA	CAASCTTCAQS	GGGTGTTGTA	660
CCGAGCTTGT	CTTCGAGGGG	TGGTGTGAAAC	TGGAGTGCCT	CTTCGCGGCG	TTTCGCCGGT	720
TTGACCGGGC	GAGCAGGCG	TGGTGCGAA	TAATGCGCTT	GTTCGCGTGG	GGCGGTTTGT	780
CCGCGATGTC	GGGGCTTGCGT	CAACGCGGAT	GCTTGCGGAG	CTTCAGCCAC	TTTCGCGCCC	840
TGGCCGCGAT	TGGGGCGCGG	TGCGGTGTTG	GAGGGCTTGTG	GGGGCTTGTG	GGGGTTCGAT	900
CGCGCTTAC	TGGCGGCGCT	CTTCGCGGAT	GGAGCTATGG	CCCTCTTGGG	GGGGTTCGCG	960
AGCAGGCGCG	CGGGCGCGTC	CAACTGGTCT	CGGGCGCGAC	GGGGCTTGTG	GGGGTTCGCG	1020
CGGGCGCGAT	GGGGCGCGAT	CTGGCGCTGT	GGGGGGGCG	GAAGGGGAGG	AGGGGGGGAC	1080
AGTACTCGGA	AAGGGGGCGG	GGGGCGCTGT	AGGGGGCGCA	GGGGCGCGCA	GGGGGGGGCA	1140
AGCGGGGGGG	TGGCGGAAAG	CTGGCTGTAC	GAAGCTCTTG	CTAACGGCGAT	GGGGGGGGCA	1200

(2) INFORMATION FOR SBC ID NO. 1438.

14. SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

MOLECULAR TYPES: proteins

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
 1 5 10 15
 Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Glu Gly Gly Ile Leu
 20 25 30 35
 Tyr Ser Ser Leu Glu Tyr Phe Glu Ilys Ala Leu Glu Glu Leu Ala Ala
 35 40 45
 Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
 50 55 60
 Gly Lys Asn Arg Asn His Val Asn Phe Phe Glu Glu Ileu Ala Asp Leu
 65 70 75 80
 Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
 85 90 95
 Thr Thr Arg Asp Ile Ieu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
 100 105 110
 Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
 115 120 125
 Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
 130 135 140
 Val Gly Gly Ala Leu Ala Tyr Ieu Val Val Iys Thr Leu Ile Asn Ala
 145 150 155 160
 Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
 165 170 175
 Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
 180 185 190
 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Ieu Asn Gly Leu Lys
 195 200 205
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
 210 215 220
 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
 225 230 235 240
 Gly Ala Thr Ser Gly Leu Ser Ala Val Thr Gly Leu Phe Gly Ala Ala
 245 250 255

Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
 260 263 270
 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Ser Gly Phe
 275 280 285
 Gly Gly Leu Pro Ser Leu Ala Glu Val His Ala Ala Ser Thr Arg Gln
 290 295 300
 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Glu Gln
 305 310 315 320
 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
 325 330 335
 Gly Gly Pro Val Gly Met Gly Met His Pro Ser Ser Gly Ala Ser
 340 345 350
 Lys Gly Thr Thr Thr Lys Lys Tyr Ser Gln Gly Ala Ala Gly Thr
 355 360 365
 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gln
 370 375 380
 Lys Val Leu Val Arg Asn Val Val
 385 390

(2) INFORMATION FOR SEQ ID NO:139:

- (I) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 439 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

ACGTTTACCC ATGGCGTCGG TGCATAGCAAC CGCCAGACAA CACAAATGGG TCTTAATTGG	60
TTATAAGCA GACATTTCGG TTGTTATGTA GAAGATGTCG ACCGATCAGA TGAAAGCATC	120
CCTGTCAGT GTTATCGGT GTCTTTTGTC ACCATCCAGC CGTGTGTTT GGCAAGCGCG	180
ACGGGGACT TGCCGCGAT CGGTACCGCC GTGAGTGTCG GGAACACAGC CGTCCTGTCG	240
CGGAGGAAGG GGTTTTAAC COCTCTGCC AATGAGCTGT CGTGTGTHAC GGCGGCGCG	300
TTCAGGCGGC ACACCAAGGA CTAGCGAGTG GTGAGTAAAGC CGGCCGGCT GGTCCATGAC	360
ATTTTCGCTGG CCTCCUGGC GGCCACCGCC GATGCGTATG CGACCAACCGA GGCGTGTAC	420
GTGTCGCGA CGTTGTAAG	439

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1441 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GAGGTTGCTG GCAATGGATT TCGGGCTTTT ACGCCCGGAA GTWAAATCAA CGCGAAATGTA	60
TTCGGTGG CGGGCGGAGT CGATGCTAGC CGCCCGCGCC GCGTGGAGG GTGTGGCGCG	120
GGAGTGTACT TGGGCCCCCG TCTGTATGG ATCGGGTGGTG TCGACAGCTGA TCUTTGGCG	180

GTGGATGAGGCG CGGGCGGCGG CGCCGATGCC GGGCCUCGCA AGCCTTATG TGCGCTGCGCT 240
 GCGGCGGCGG GGGGGGGGGG CGAAGGAGAC AGGACCAAGG GGGGGGGGGG CGGGGGGAGG 300
 GTTGGGAGAC GGGTTGGGGA TGGAGGCGG AGACATCCCTC GTCCGGGGCGA ACCGGCGGG 360
 GTTGATGTCG CTGGTCGCGG CGAACATCTC GGAGGAAAC AGTGGCGGCA TGCGGCTAC 420
 CCGGGCGGCGA TATGGCGGAA TTGTGGGGCA AGAGCTCTGG CGTAGTATACA GCTATGGGG 480
 GCGAATCTCG GCGGGGGGGG GTTGGGGGGG GTTGGGGGGG CGGGGGGGGG CGGGGGGGGG 540
 GGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG 600
 TGGAGGCGGG AGACTGGGGG AGCTGGGGGG AGGGGGGGGG AGGGGGGGGG AGGGGGGGGG 660
 GGGGGGGGG AGCTGGGGGG AGGGGGGGGG AGGGGGGGGG AGGGGGGGGG AGGGGGGGGG 720
 GCGAACGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG 780
 CGGGGGGGGG ATGGGGGGGG AGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG 840
 CGGGGGGGGG ATGGGGGGGG AGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG 900
 CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG 960
 TGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG 1020
 CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG 1080
 CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG 1140
 CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG 1200
 CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG 1260
 CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG 1320
 CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG 1380
 CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG 1440
 G

(2) INFORMATION FOR SSO ID NO. 143

1.3. SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

Molecular-type protein

(x) SEQUENCE DESCRIPTION: SEQ ID NO:161:

(2) INFORMATION FOR SEQ ID NO:142

6.2 SEQUENCE CHARACTERISTICS

- (A) LENGTH: 423 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(iii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr
 1 9 10 19
 Ser Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Ala Trp Asp
 20 25 30
 Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val
 35 40 45
 Val Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala
 50 55 60
 Met Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala
 65 70 75 80
 Ala Leu Ala Lys Gln Thr Ala Thr Gln Ala Arg Ala Ala Ala Gln Ala
 85 90 95
 Phe Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala
 100 105 110
 Asn Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln
 115 120 125
 Asn Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp
 130 135 140
 Ala Gln Asp Ala Ala Val Met Tyr Ser Tyr Gln Gly Ala Ser Ala Ala
 145 150 155 160
 Ala Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro
 165 170 175
 Ala Gly Pro Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly
 180 185 190
 Ala Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile
 195 200 205
 Leu Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr
 210 215 220
 Ser Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser
 225 230 235 240
 Ala Gln Pro Ile Val Pro Thr Pro Ile Gly Glu Leu Asp Val Ile
 245 250 255
 Ala Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile
 260 265 270
 Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly
 275 280 285
 Gly Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu
 290 295 300
 Pro Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala
 305 310 315 320
 Gly Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser
 325 330 335
 Trp Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro
 340 345 350
 Thr Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met
 355 360 365
 Pro Ala Gly Ileu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg
 370 375 380

Gly Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly
 185 390 385 400
 Gin Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro
 405 410 415
 Pro Pro Gly Asn Pro Pro Arg
 420

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
 1 5 10 15
 Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
 20 25 30
 Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
 35 40 45
 Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys
 50 55 60
 Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Gln Ala Ala
 65 70 75 80
 Gly Thr Tyr Val Ala Ala Asp Ala Ala Ser Thr Tyr Thr Gly
 85 90 95
 Phe

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Cys Arg Leu Cys Leu Asp Ser His Leu Arg Val Val Ala Leu Pro Ala
 1 5 10 15
 Gly Gln Pro Gly Arg Leu Val Gln Ala Ile Gly Pro Ala Gln Glu Arg
 20 25 30
 Asp Val Gly Gln Thr Arg Cys Thr Arg Thr Gly Leu Asp Xaa Val Ser
 35 40 45
 Ala Leu Thr Ala Ala Gln Phe Ala Ala His Ala Gln Ile Tyr Gln Ala
 50 55 60
 Val Ser Ala Gln Ala Ala Ile His Gln Met Phe Val Asn Thr Leu

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65 70 75 80
 Gln Xaa Xaa Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Asn Asx Ala
 85 90 95
 Ala Ala Gly

Claims

1. A polypeptide comprising an immunogenic portion of a *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID NO:1, 11, 12, 83, 103-108, 125, 127, 129-137, 139 and 140, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NO: 1, 11, 12, 83, 103-108, 125, 127, 129-137, 139 and 140, or a complement thereof under moderately stringent conditions.
2. A polypeptide comprising an immunogenic portion of a *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NO: 16-33, 109, 126, 138, 141, 142 and variants thereof.
3. A DNA molecule comprising a nucleotide sequence encoding a polypeptide according to any one of claims 1 and 2.
4. An expression vector comprising a DNA molecule according to claim 3.
5. A host cell transformed with an expression vector according to claim 4.
6. The host cell of claim 5 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cells.
7. A pharmaceutical composition comprising at least one polypeptide according to any one of claims 1 and 2 and a physiologically acceptable carrier.

8. A pharmaceutical composition comprising at least one DNA molecule according to claim 3 and a physiologically acceptable carrier.

9. A pharmaceutical composition comprising at least one DNA molecule having a sequence recited in SEQ ID NO: 2-10, 102, 128, and a physiologically acceptable carrier.

10. A vaccine comprising at least one polypeptides according to any one of claims 1 and 2 and a non-specific immune response enhancer.

11. A vaccine comprising:

at least one polypeptide encoded by a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NO: 2-10, 102, 128; and
a non-specific immune response enhancer.

12. The vaccine of claims 10-11 wherein the non-specific immune response enhancer is an adjuvant.

13. A vaccine comprising at least one DNA molecules according to claim 3 and a non-specific immune response enhancer.

14. A vaccine comprising at least one DNA molecule having a sequence recited in SEQ ID NO: 2-10, 102, 128; and a non-specific immune response enhancer.

15. The vaccine of claims 13 or 14 wherein the non-specific immune response enhancer is an adjuvant.

16. A method for inducing protective immunity in a patient, comprising administering to a patient a pharmaceutical composition according to any one of claims 7-9.

17. A method for inducing protective immunity in a patient, comprising administering to a patient a vaccine according to any one of claims 10-13.

18. A fusion protein comprising at least two polypeptides according to any one of claims 1 and 2.

19. A fusion protein comprising a polypeptide according to any one of claims 1 and 2 and a known *M. tuberculosis* antigen.

20. A pharmaceutical composition comprising a fusion protein according to any one of claims 18 and 19, and a physiologically acceptable carrier.

21. A vaccine comprising a fusion protein according to any one of claims 18 and 19, and a non-specific immune response enhancer.

22. The vaccine of claim 21 wherein the non-specific immune response enhancer is an adjuvant.

23. A method for inducing protective immunity in a patient, comprising administering to a patient a pharmaceutical composition according to claim 20.

24. A method for inducing protective immunity in a patient, comprising administering to a patient a vaccine according to any one of claims 21 and 22.

25. A method for detecting tuberculosis in a patient, comprising:

(a) contacting dermal cells of a patient with at least one polypeptide according to any one of claims 1 and 2; and

(b) detecting an immune response on the patient's skin and therefrom detecting tuberculosis in the patient.

26. A method for detecting tuberculosis in a patient, comprising:

- (a) contacting dermal cells of a patient with at least one polypeptide encoded by a DNA sequence selected from the group consisting of SEQ ID NO:2-10, 102, 128, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NO:2-10, 102, 128; and
- (b) detecting an immune response on the patient's skin and therefrom detecting tuberculosis in the patient.

27. The method of any one of claims 25 and 26 wherein the immune response is induration.

28. A diagnostic kit comprising:

- (a) a polypeptide according to any one of claims 1 and 2; and
- (b) apparatus sufficient to contact said polypeptide with the dermal cells of a patient.

29. A diagnostic kit comprising:

- (a) a polypeptide encoded by a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NO: 2-10, 102, 128; and
- (b) apparatus sufficient to contact said polypeptide with the dermal cells of a patient.

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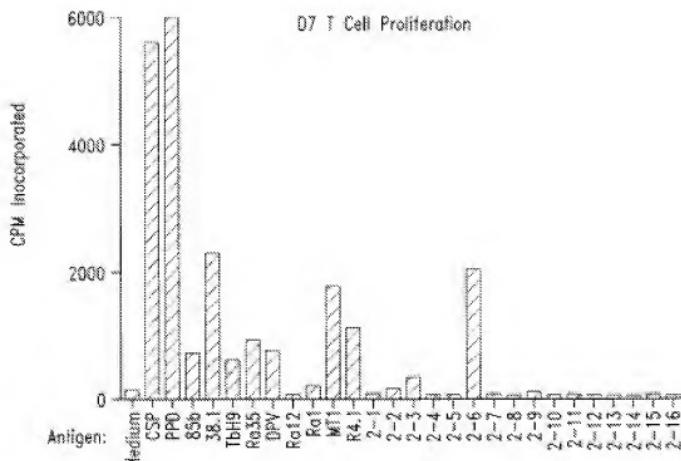


Fig. 1A

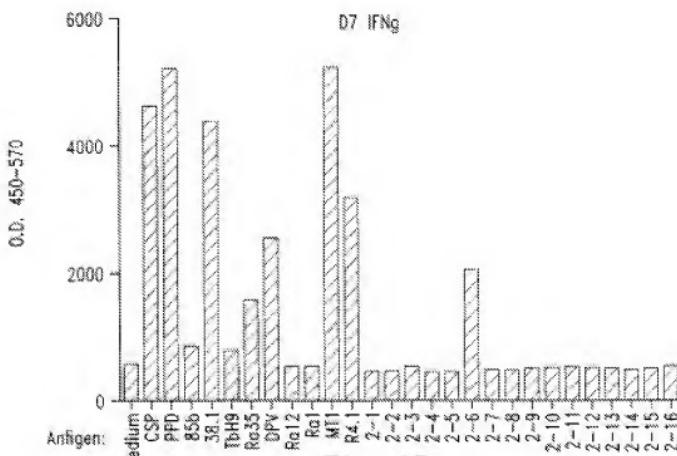


Fig. 1B

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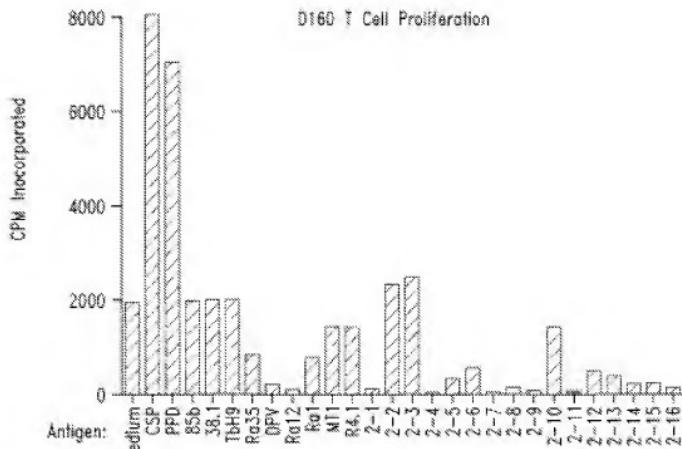


Fig. 2A

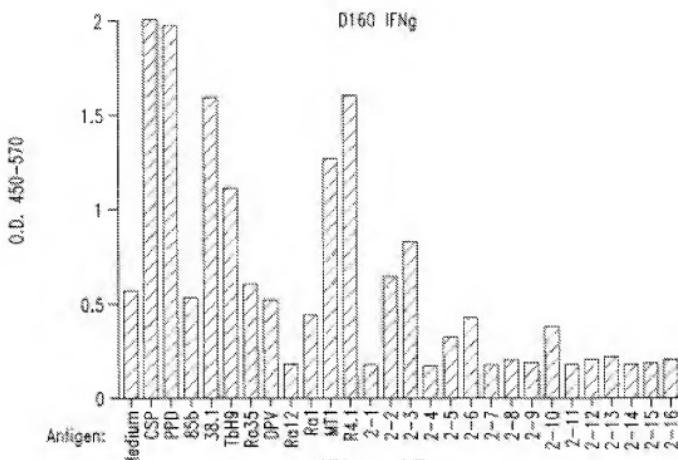


Fig. 2B